



# SEQUENCE LISTING

<110> LEE, Sang-Yup  
JEONG, Ki-Jun

<120> ESCHERICHIA COLI STRAIN SECRETING HUMAN  
GRANULOCYTE COLONY STIMULATING FACTOR (G-CSF)

<130> HYLEE60.001APC

<140> US 10/009,792

<141> 2001-11-13

<150> PCT/KR01/00549

<151> 2001-03-31

<150> KR 10-2000-0017052

<151> 2000-03-31

<160> 27

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5

10

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gcgaattcat ggctggacct gccacccag

29

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<211> 32

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 tcctcggggg ggcacagctt gtaggtggca cacagcttct cctggagcgc 50

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<400> 7  
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<400> 13  
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<210> 14  
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<400> 14  
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<210> 15  
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<400> 15  
 caccatcacc atatcgaagg ccgtactccg ttaggtcca 39

<210> 16  
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 <212> DNA  
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<400> 16  
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 agcttcctgc tcaagtgtt agagcaagtg aggaagatcc agggcgatgg cgcagcgctc 180  
 caggagaagc tggcaggctg cttgagccaa ctccatagcg gccttttct ctaccagggg 240  
 ctctgcagg ccctggaagg gatctcccc gagttgggtc ccaccttggg cactctgcag 300  
 ctggacgtcg ccgactttgc caccaccatc tggcagcaga tggagaact gggaatggcc 360  
 cctgcctgc agccaccca gggtgccatg ccggccttcg cctctgcttt ccagcgccg 420  
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 ctacgccacc ttgcccagcc ctaataa 507

<210> 18  
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 <212> DNA  
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 agtgcactct ggacagtgca ggaagccacc ccctggggc ctgccagctc cctgccccag 120  
 agcttcctgc tcaagtgtt agagcaagtg aggaagatcc agggcgatgg cgcagcgctc 180  
 caggagaagc tgtgtgccac ctacaagctg tgccaccccg aggagctggt gctgctcgga 240  
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 gcaggtgct tgagccaact ccatagcggc ctttctctt accaggggt cctgcaggcc 360  
 ctggaaggga tctccccga gttgggtccc acctggaca cactgcagct ggacgtcgcc 420  
 gactttgcca ccaccatctg gcagcagatg gaagaactgg gaatggcccc tgccctgcag 480  
 cccaccaggt gtgccatgcc ggccttcgcc tctgctttcc agcgccgggc aggaggggtc 540  
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 gccagccct aataa 615

<210> 19  
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<400> 19  
 Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys  
 1 5 10 15  
 Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln  
 20 25 30  
 Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val  
 35 40 45  
 Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys  
 50 55 60  
 Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser  
 65 70 75 80  
 Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser  
 85 90 95  
 Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp  
 100 105 110  
 Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro  
 115 120 125  
 Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe  
 130 135 140  
 Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe  
 145 150 155 160  
 Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro  
 165 170

<210> 20  
 <211> 531  
 <212> DNA  
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<400> 20  
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caagtgagga agatccag agatggcgca gcgctccagg agaagctgtg ccacctac 120  
 aagctgtgcc accccgagg gctggtgctg ctcggacact ctctgggcat cccctgggct 180  
 cccctgagca gctgccccag ccaggccctg cagctggcag gctgcttgag ccaactccat 240  
 agcggccttt tcctctacca ggggctcctg caggccctgg aagggatctc ccccgagttg 300  
 ggtccacact tggacacact gcagctggac gtcgccgact ttgccaccac catctggcag 360  
 cagatggaag aactgggaat ggccccctgcc ctgcagccca cccagggtgc catgccggcc 420  
 ttcgcctctg ctttcagcg ccgggcagga ggggtcctag ttgcctcca tctgcagagc 480  
 ttctggagg tgcgtaccg cgttctacgc caccttgccc agcctaata a 531

<210> 21  
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<400> 21  
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 1 5 10 15  
 Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu  
 20 25 30  
 Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu  
 35 40 45  
 Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser  
 50 55 60  
 Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His  
 65 70 75 80  
 Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile  
 85 90 95  
 Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala  
 100 105 110  
 Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala  
 115 120 125  
 Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala  
 130 135 140  
 Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser  
 145 150 155 160  
 Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro  
 165 170 175

<210> 22  
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<400> 22  
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<210> 23  
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 <212> PRT  
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<400> 23  
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<210> 24  
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<400> 24  
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 ttctgctca agtgc 135

<210> 25  
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<400> 25  
 Met Phe Lys Phe Lys Lys Lys Phe Leu Val Gly Leu Thr Ala Ala Phe  
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 Met Ser Ile Ser Met Phe Ser Ala Thr Ala Ser Ala Thr Pro Leu Gly  
 20 25 30  
 Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys  
 35 40 45

<210> 26  
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 <212> DNA  
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<400> 26  
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 atgttttctg caaccgcctc tgcagctggc ccgcaccatc accatcacca tatcgaggga 120  
 aggactccgt taggtccagc cagctccctg ccccagagct tctgctcaa gtgcttagag 180

<210> 27  
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<400> 27  
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 Met Ser Ile Ser Met Phe Ser Ala Thr Ala Ser Ala Ala Gly Pro His  
 20 25 30  
 His His His His His Ile Glu Gly Arg Thr Pro Leu Gly Pro Ala Ser  
 35 40 45  
 Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu  
 50 55 60